

#10

1600

1644

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/500,746

DATE: 10/18/2001
TIME: 09:45:14

Input Set : A:\ES.txt
Output Set: N:\CRF3\10182001\I500746.raw

ENTERED

3 <110> APPLICANT: Winchester , Robert J.
4 Gulko, Percio
5 Seki, Tetsunori
7 <120> TITLE OF INVENTION: USES OF INHIBITORS FOR THE ACTIVATION OF CXCR4 RECEPTOR BY
SDF-1 IN
8 TREATING RHEVMATOID ARTHRITIS
10 <130> FILE REFERENCE: 0575/57005-B
12 <140> CURRENT APPLICATION NUMBER: 09/500,746
13 <141> CURRENT FILING DATE: 2000-02-09
15 <160> NUMBER OF SEQ ID NOS: 23
17 <170> SOFTWARE: PatentIn version 3.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 13
21 <212> TYPE: DNA
22 <213> ORGANISM: Artificial Sequence
24 <220> FEATURE:
25 <223> OTHER INFORMATION: Primer
27 <220> FEATURE:
28 <221> NAME/KEY: misc_feature
29 <223> OTHER INFORMATION: primer
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33 gatccgcggc cgc 13
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38 <212> TYPE: DNA
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56 <213> ORGANISM: Artificial Sequence
58 <220> FEATURE:
59 <223> OTHER INFORMATION: Primer
61 <220> FEATURE:
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63 <223> OTHER INFORMATION: Primer
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70 <210> SEQ ID NO: 4
71 <211> LENGTH: 12
72 <212> TYPE: DNA
73 <213> ORGANISM: Artificial Sequence

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76 <223> OTHER INFORMATION: Primer
78 <220> FEATURE:
79 <221> NAME/KEY: misc_feature
80 <223> OTHER INFORMATION: Primer
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87 <210> SEQ ID NO: 5
88 <211> LENGTH: 24
89 <212> TYPE: DNA
90 <213> ORGANISM: Artificial Sequence
92 <220> FEATURE:
93 <223> OTHER INFORMATION: Primer
95 <220> FEATURE:
96 <221> NAME/KEY: misc_feature
97 <223> OTHER INFORMATION: Primer
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104 <210> SEQ ID NO: 6
105 <211> LENGTH: 12
106 <212> TYPE: DNA
107 <213> ORGANISM: Artificial Sequence
109 <220> FEATURE:
110 <223> OTHER INFORMATION: Primer
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113 <221> NAME/KEY: misc_feature
114 <223> OTHER INFORMATION: Primer
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118 gatcctccct cg 12
121 <210> SEQ ID NO: 7
122 <211> LENGTH: 24
123 <212> TYPE: DNA
124 <213> ORGANISM: Artificial Sequence
126 <220> FEATURE:
127 <223> OTHER INFORMATION: Primer
129 <220> FEATURE:
130 <221> NAME/KEY: misc_feature
131 <223> OTHER INFORMATION: Primer
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141 <213> ORGANISM: Artificial Sequence
143 <220> FEATURE:
144 <223> OTHER INFORMATION: Primer
146 <220> FEATURE:
147 <221> NAME/KEY: misc_feature
148 <223> OTHER INFORMATION: Primer

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151 <400> SEQUENCE: 8
152 gatacctcggt ga
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160 <220> FEATURE:
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162 <222> LOCATION: (337)..(337)
163 <223> OTHER INFORMATION: x= to any amino acid
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167 <221> NAME/KEY: MISC_FEATURE
168 <222> LOCATION: (376)..(376)
169 <223> OTHER INFORMATION: x= to any amino acid
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175 1 5 10 15
178 Gly Pro Phe Ala His Lys Glu Gly Pro Asn His Gln Leu Ile Ser Tyr
179 20 25 30
182 Gln Gly Arg Ile Pro Tyr Pro Arg Ser Ala Val Cys Val Tyr His Leu
183 35 40 45
186 Ser Asp Ile Gln Thr Val Phe Asn Gly Pro Phe Ala His Lys Glu Gly
187 50 55 60
190 Pro Asn His Gln Leu Ile Ser Tyr Gln Gly Arg Ile Pro Tyr Pro Arg
191 65 70 75 80
194 Ser Ala Val Cys Val Tyr Ser Met Ala Asp Ile Arg Met Val Phe Asn
195 85 90 95
198 Gly Pro Phe Ala His Lys Glu Gly Pro Asn Tyr Gln Trp Met Pro Phe
199 100 105 110
202 Ser Gly Lys Met Pro Tyr Pro Arg Ser Ala Val Cys Val Tyr Ser Met
203 115 120 125
206 Asn Asp Val Arg Arg Ala Phe Leu Gly Pro Phe Ala His Lys Glu Gly
207 130 135 140
210 Pro Met His Gln Trp Val Ser Tyr Gln Gly Arg Val Pro Tyr Pro Arg
211 145 150 155 160
214 Ser Ala Val Cys Met Tyr Ser Met Ser Asp Val Arg Arg Val Arg Arg
215 165 170 175
218 Val Phe Leu Gly Pro Tyr Ala His Arg Asp Gly Pro Asn Tyr Gln Trp
219 180 185 190
222 Val Pro Tyr Gln Gly Arg Val Pro Tyr Pro Arg Pro Gly Thr Cys Pro
223 195 200 205
226 Gly Gly Ala Phe Thr Pro Asn Met Arg Thr Thr Lys Asp Phe Pro Asp
227 210 215 220
230 Asp Val Val Thr Phe Ile Arg Asn His Pro Leu Met Tyr Asn Ser Ile
231 225 230 235 240
234 Ser Pro Ile Pro Gly Thr Cys Pro Gly Gly Ala Leu Thr Pro Asn Met
235 245 250 255
238 Arg Thr Thr Lys Glu Phe Pro Asp Asp Val Val Thr Phe Ile Arg Asn
239 260 265 270

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12

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242 His Pro Leu Met Tyr Asn Ser Ile Tyr Pro Ile Pro Gly Thr Cys Pro
243      275      280      285
246 Gly Gly Thr Phe Thr Pro Ser Met Lys Ser Thr Lys Asp Tyr Pro Asp
247      290      295      300
250 Glu Val Ile Asn Phe Met Arg Ser His Pro Leu Met Tyr Gln Ala Val
251 305      310      315      320
254 Tyr Pro Leu Pro Gly Met Cys Pro Ser Lys Thr Phe Gly Thr Phe Ser
255      325      330      335
W--> 258 Xaa Ser Thr Lys Asp Phe Pro Asp Asp Val Ile Phe Ala Arg Asn His
259      340      345      350
262 Pro Leu Met Tyr Asn Ser Val Leu Pro Thr Pro Gly Thr Cys Pro Ser
263      355      360      365
W--> 266 Lys Thr Phe Gly Gly Phe Asp Xaa Ser Thr Lys Asp Leu Pro Asp Asp
267      370      375      380
270 Val Ile Thr Phe Ala Arg Ser His Pro Ala Met Tyr Asn Pro Val Phe
271 385      390      395      400
274 Pro Met His Arg Arg Pro Leu Ile Val Arg Ile Gly Thr Asp Tyr Lys
275      405      410      415
278 Tyr Thr Lys Ile Ala Val Asp His Lys Arg Pro Leu Ile Val Arg Ile
279      420      425      430
282 Gly Thr Asp Tyr Lys Tyr Thr Lys Ile Ala Val Asp Gln Arg Arg Pro
283      435      440      445
286 Leu Val Val Arg Thr Gly Ala Pro Tyr Arg Leu Thr Thr Ile Ala Val
287      450      455      460
290 Asp Gly Gly Arg Pro Leu Phe Leu Gln Val Gly Ala Asn Tyr Thr Phe
291 465      470      475      480
294 Thr Gln Ile Ala Ala Asp Asn Asn Arg Pro Ile Val Ile Lys Thr Asp
295      485      490      495
298 Val Asn Tyr Gln Phe Thr Gln Ile Val Val Asp
299      500      505
302 <210> SEQ ID NO: 10
303 <211> LENGTH: 396
304 <212> TYPE: PRT
305 <213> ORGANISM: Human
307 <400> SEQUENCE: 10
309 Ser Tyr Pro Ala Pro His Gly Pro Glu Asp Pro Ala Pro Gln Phe Ala
310 1      5      10      15
313 His Met Phe Glu Asn Glu Ile Ser His Arg Thr Gly Ser Trp Asn Phe
314      20      25      30
317 Ala Pro Asn Pro Asp Lys Gln Trp Leu Leu Gln Arg Thr Ser His Ala
318      35      40      45
321 Ala Pro His Gly Pro Glu Asp Ser Ala Pro Gln Phe Ser Glu Leu Tyr
322      50      55      60
325 Pro Asn Ala Ser Gln His Ile Thr Pro Ser Tyr Asn Tyr Ala Pro Asn
326 65      70      75      80
329 Met Asp Lys His Trp Ile Met Gln Tyr Thr Ala Thr Pro Ala Pro His
330      85      90      95
333 Ser Pro Trp Thr Ala Ala Pro Gln Tyr Gln Lys Ala Phe Gln Asn Val
334      100      105      110

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337 Phe Ala Pro Arg Asn Lys Asn Phe Asn Ile His Gly Thr Asn Lys His
338      115      120      125
341 Trp Leu Ile Arg Gln Ala Lys Gly Lys Met Asn Asp Val His Ile Ser
342      130      135      140
345 Phe Thr Asp Leu Leu His Arg Arg Arg Leu Gln Thr Leu Gln Ser Val
346 145      150      155      160
349 Asp Glu Gly Ile Glu Arg Leu Phe Asn Leu Leu Arg Glu Leu Asn Gln
350      165      170      175
353 Leu Trp Asn Thr Gly Pro Met Leu Pro Ile His Met Glu Phe Thr Asn
354      180      185      190
357 Ile Leu Gln Arg Lys Arg Leu Gln Thr Leu Met Ser Val Asp Asp Ser
358      195      200      205
361 Val Glu Arg Leu Tyr Asn Met Leu Val Glu Thr Gly Glu Leu Glu Asn
362      210      215      220
365 Thr Thr Pro Met Thr Asn Ser Ser Ile Gln Phe Leu Asp Asn Ala Phe
366 225      230      235      240
369 Arg Lys Arg Trp Gln Thr Leu Leu Ser Val Asp Asp Leu Val Glu Lys
370      245      250      255
373 Leu Val Lys Arg Leu Glu Phe Thr Gly Glu Leu Asn Asn Thr Tyr Ala
374      260      265      270
377 Ile Tyr Thr Ser Asp His Gly Tyr His Leu Gly Gln Phe Gly Leu Leu
378      275      280      285
381 Lys Gly Lys Asn Met Pro Tyr Glu Phe Asp Ile Arg Val Pro Phe Phe
382      290      295      300
385 Met Arg Gly Pro Gly Ile Pro Arg Tyr Ile Ile Tyr Thr Ala Asp His
386 305      310      315      320
389 Gly Tyr His Ile Gly Gln Phe Gly Leu Val Lys Gly Lys Ser Met Pro
390      325      330      335
393 Tyr Asp Phe Asp Ile Arg Val Pro Phe Phe Ile Arg Gly Pro Ser Val
394      340      345      350
397 Glu Pro Tyr Ile Phe Tyr Thr Ser Asp Asn Gly Tyr His Thr Gly Gln
398      355      360      365
401 Phe Ser Leu Pro Ile Asp Lys Arg Gln Leu Tyr Glu Phe Asp Ile Lys
402      370      375      380
405 Val Pro Leu Leu Val Arg Gly Pro Gly Ile Lys Pro
406 385      390      395
409 <210> SEQ ID NO: 11
410 <211> LENGTH: 102
411 <212> TYPE: PRT
412 <213> ORGANISM: Human
414 <400> SEQUENCE: 11
416 Ser Ala Val Cys Val Tyr Tyr Ser Met Ala Asp Ile Arg Met Val Phe
417 1      5      10      15
420 Asn Gly Pro Phe Ala His Lys Glu Gly Pro Asn Tyr Gln Trp Met Pro
421      20      25      30
424 Phe Ser Gly Lys Met Pro Tyr Pro Arg Pro Gly Thr Cys Pro Gly Gly
425      35      40      45
428 Thr Phe Thr Pro Ser Met Lys Ser Thr Lys Asx Tyr Pro Asp Glu Val
429      50      55      60

```


 Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:258 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:266 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:469 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:510 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1240 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1244 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1256 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1340 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23